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RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/062,375

TIME: 09:30:31

Input Set : N:\Crf3\RULE60\10062375.raw

Output Set: N:\CRF3\03262002\J062375.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Sutcliffe, Gregor J.  
6 de Lecea, Luis  
7 Siggins, George R.  
8 Henriksen, Steven J.

10 (ii) TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,  
11 COMPOSITIONS AND METHODS

13 (iii) NUMBER OF SEQUENCES: 26

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
17 (B) STREET: 10666 North Torrey Pines Road, TPC-8  
18 (C) CITY: La Jolla  
19 (D) STATE: California  
20 (E) COUNTRY: US  
21 (F) ZIP: 92037

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/062,375  
C--> 31 (B) FILING DATE: 30-Jan-2002  
32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/857,389  
36 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Schmonsees, William  
41 (B) REGISTRATION NUMBER: 31,796  
42 (C) REFERENCE/DOCKET NUMBER: 22908-0002

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (415) 324-7041  
46 (B) TELEFAX: (415) 324-0638

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 438 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

ENTERED

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61 (iv) ANTI-SENSE: NO

63 (ix) FEATURE:

64 (A) NAME/KEY: CDS

65 (B) LOCATION: 30..368

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

70	AAAGCACAGA	CTTCAGGTTT	CCAAGGAGG	ATG	GGT	GGC	TGC	AGC	ACA	AGA	GGC	53
71				Met	Gly	Gly	Cys	Ser	Thr	Arg	Gly	
72				1				5				
74	AAG	CGG	CCG	TCA	GCC	CTC	AGT	CTG	CTG	CTG	CTG	101
75	Lys	Arg	Pro	Ser	Ala	Leu	Ser	Leu	Leu	Leu	Leu	
76	10			15				20				
78	ATC	GCA	GCC	TCT	GCC	CTC	CCC	CTG	GAG	AGC	GGT	149
79	Ile	Ala	Ala	Ser	Ala	Leu	Pro	Leu	Glu	Ser	Gly	
80	25			30				35			40	
82	AGT	GTG	CAG	GAT	GCC	ACA	GGC	GGG	AGG	AGG	ACC	197
83	Ser	Val	Gln	Asp	Ala	Thr	Gly	Gly	Arg	Arg	Thr	
84				45				50			55	
86	CTT	GCC	TGG	TGG	CAT	GAG	TGG	GCT	TCC	CAA	GAC	245
87	Leu	Ala	Trp	Trp	His	Glu	Trp	Ala	Ser	Gln	Asp	
88			60					65			70	
90	TTC	GAA	GGG	GGT	ACC	CCG	GAG	CTG	TCT	AAG	CGG	293
91	Phe	Glu	Gly	Gly	Thr	Pro	Glu	Leu	Ser	Lys	Arg	
92			75					80			85	
94	CTC	CAG	CAG	CCC	CCA	CAC	CGG	GAT	AAA	AAG	CCC	341
95	Leu	Gln	Gln	Pro	Pro	His	Arg	Asp	Lys	Lys	Pro	
96			90					95			100	
98	TGG	AAA	ACC	TTC	TCC	TCG	TGC	AAG	TAGCCCGAGC	CTGACCGGAG	CCTGACCGGC	395
99	Trp	Lys	Thr	Phe	Ser	Ser	Cys	Lys				
100	105			110								
102	CACCCTGTGA	ATGCAGCCGT	GGCCTGAATA	AAGAGTGTCA	AGT							438

105 (2) INFORMATION FOR SEQ ID NO: 2:

107 (i) SEQUENCE CHARACTERISTICS:

108 (A) LENGTH: 112 amino acids

109 (B) TYPE: amino acid

110 (D) TOPOLOGY: linear

112 (ii) MOLECULE TYPE: protein

113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

115	Met	Gly	Gly	Cys	Ser	Thr	Arg	Gly	Lys	Arg	Pro	Ser	Ala	Leu	Ser	Leu
116	1			5				10						15		
118	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Gly	Ile	Ala	Ala	Ser	Ala	Leu	Pro	Leu
119			20					25						30		
121	Glu	Ser	Gly	Pro	Thr	Gly	Gln	Asp	Ser	Val	Gln	Asp	Ala	Thr	Gly	Gly
122			35					40					45			
124	Arg	Arg	Thr	Gly	Leu	Leu	Thr	Phe	Leu	Ala	Trp	Trp	His	Glu	Trp	Ala
125			50					55					60			
127	Ser	Gln	Asp	Ser	Ser	Ser	Thr	Ala	Phe	Glu	Gly	Gly	Thr	Pro	Glu	Leu
128	65							70					75			80
130	Ser	Lys	Arg	Gln	Glu	Arg	Pro	Pro	Leu	Gln	Gln	Pro	Pro	His	Arg	Asp
131				85				90						95		

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133 Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 134 100 105 110

140 (2) INFORMATION FOR SEQ ID NO: 3:  
 142 (i) SEQUENCE CHARACTERISTICS:  
 143 (A) LENGTH: 110 amino acids  
 144 (B) TYPE: amino acid  
 145 (D) TOPOLOGY: linear  
 147 (ii) MOLECULE TYPE: protein  
 149 (v) FRAGMENT TYPE: C-terminal  
 153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 155 Gln Cys Ala Leu Ala Ala Leu Cys Ile Val Leu Ala Leu Gly Gly Val  
 156 1 5 10 15  
 158 Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser  
 159 20 25 30  
 161 Leu Ala Ala Ala Thr Gly Lys Gln Glu Leu Ala Lys Tyr Phe Leu Ala  
 162 35 40 45  
 164 Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu Asn Asp Ala Leu Glu Pro  
 165 50 55 60  
 167 Glu Asp Leu Pro Gln Ala Ala Glu Gln Asp Glu Met Arg Leu Glu Leu  
 168 65 70 75 80  
 170 Gln Arg Ser Ala Asn Ser Asn Pro Ala Met Ala Pro Arg Glu Arg Lys  
 171 85 90 95  
 172 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys  
 173 100 105 110

175 (2) INFORMATION FOR SEQ ID NO: 4:  
 177 (i) SEQUENCE CHARACTERISTICS:  
 178 (A) LENGTH: 427 base pairs  
 179 (B) TYPE: nucleic acid  
 180 (C) STRANDEDNESS: single  
 181 (D) TOPOLOGY: linear  
 183 (ii) MOLECULE TYPE: cDNA  
 185 (iii) HYPOTHETICAL: NO  
 187 (iv) ANTI-SENSE: NO  
 190 (ix) FEATURE:  
 191 (A) NAME/KEY: CDS  
 192 (B) LOCATION: 25..354

195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 197 GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC 51  
 198 Met Met Gly Gly Arg Gly Thr Gly Gly  
 199 1 5  
 201 AAG TGG CCC TCA GCC TTC GGG CTG CTG CTG CTC TGG GGG GTC GCA GCC 99  
 202 Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala  
 203 10 15 20 25  
 205 TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG 147  
 206 Ser Ala Leu Pro Ser Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln  
 207 30 35 40  
 209 GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG 195  
 210 Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp  
 211 45 50 55

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213 CAC GAG TGG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT 243  
 214 His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly  
 215 60 65 70  
 217 ACC CCC GGG CTG TCC AAG AGC CAG GAA AGG CCA CCC CCC CAA CAG CCC 291  
 218 Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro  
 219 75 80 85  
 221 CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC 339  
 222 Pro His Leu Asp Lys Pro Cys Lys Asn Phe Trp Lys Thr Phe  
 223 90 95 100 105  
 224 TCC TCG TGC AAG TAACCCACCT CTGGGCATAG CACCCTGGCC ACCCTGTGAG 391  
 225 Ser Ser Cys Lys  
 W--> 226 110  
 228 ATGCCAACGA GACCTGAATA AAGACTGTCA ATCAAC 427  
 231 (2) INFORMATION FOR SEQ ID NO: 5:  
 233 (i) SEQUENCE CHARACTERISTICS:  
 234 (A) LENGTH: 109 amino acids  
 235 (B) TYPE: amino acid  
 236 (D) TOPOLOGY: linear  
 238 (ii) MOLECULE TYPE: protein  
 240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 242 Met Met Gly Gly Arg Gly Thr Gly Gly Lys Trp Pro Ser Ala Phe Gly  
 243 1 5 10 15  
 245 Leu Leu Leu Leu Trp Gly Val Ala Ala Ser Ala Leu Pro Leu Glu Ser  
 246 20 25 30  
 248 Gly Pro Thr Gly Gln Asp Ser Val Gln Glu Ala Thr Glu Gly Arg Ser  
 249 35 40 45  
 251 Gly Leu Leu Thr Phe Leu Ala Trp Trp His Glu Trp Ala Ser Gln Ala  
 252 50 55 60  
 254 Ser Ser Ser Thr Pro Val Gly Gly Gly Thr Pro Gly Leu Ser Lys Ser  
 255 65 70 75 80  
 257 Gln Glu Arg Pro Pro Pro Gln Gln Pro Pro His Leu Asp Lys Lys Pro  
 258 85 90 95  
 260 Cys Lys Asn Phe Trp Lys Thr Phe Ser Ser Cys Lys  
 261 100 105  
 264 (2) INFORMATION FOR SEQ ID NO: 6:  
 266 (i) SEQUENCE CHARACTERISTICS:  
 267 (A) LENGTH: 85 amino acids  
 268 (B) TYPE: amino acid  
 269 (D) TOPOLOGY: linear  
 271 (ii) MOLECULE TYPE: protein  
 273 (v) FRAGMENT TYPE: C-terminal  
 277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 279 Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln  
 280 1 5 10 15  
 281 Asp Ala Thr Gly Gly Arg Arg Thr Gly Leu Leu Thr Phe Leu Ala Trp  
 282 20 25 30  
 284 Trp His Glu Trp Ala Ser Gln Asp Ser Ser Ser Thr Ala Phe Glu Gly  
 285 35 40 45  
 287 Gly Thr Pro Glu Leu Ser Lys Arg Gln Glu Arg Pro Pro Leu Gln Gln

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 Output Set: N:\CRF3\03262002\J062375.raw

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288          50          55          60
290    Pro Pro His Arg Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr
291      65          70          75          80
293    Phe Ser Ser Cys Lys
294          85
296 (2) INFORMATION FOR SEQ ID NO: 7:
298   (i) SEQUENCE CHARACTERISTICS:
299       (A) LENGTH: 29 amino acids
300       (B) TYPE: amino acid
301       (D) TOPOLOGY: linear
303   (ii) MOLECULE TYPE: protein
305   (v) FRAGMENT TYPE: C-terminal
309   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
311    Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp Lys Lys Pro
312      1          5          10          15
314    Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
315      20          25
317 (2) INFORMATION FOR SEQ ID NO: 8:
319   (i) SEQUENCE CHARACTERISTICS:
320       (A) LENGTH: 14 amino acids
321       (B) TYPE: amino acid
322       (D) TOPOLOGY: linear
324   (ii) MOLECULE TYPE: protein
326   (v) FRAGMENT TYPE: C-terminal
330   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
332    Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe Ser Ser Cys Lys
333      1          5          10
335 (2) INFORMATION FOR SEQ ID NO: 9:
337   (i) SEQUENCE CHARACTERISTICS:
338       (A) LENGTH: 13 amino acids
339       (B) TYPE: amino acid
340       (D) TOPOLOGY: linear
342   (ii) MOLECULE TYPE: protein
344   (v) FRAGMENT TYPE: internal
348   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
350    Gln Glu Arg Pro Pro Leu Gln Gln Pro Pro His Arg Asp
351      1          5          10
353 (2) INFORMATION FOR SEQ ID NO: 10:
355   (i) SEQUENCE CHARACTERISTICS:
356       (A) LENGTH: 84 amino acids
357       (B) TYPE: amino acid
358       (D) TOPOLOGY: linear
360   (ii) MOLECULE TYPE: protein
362   (v) FRAGMENT TYPE: C-terminal
366   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
368    Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln
369      1          5          10          15
371    Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp
372      20          25          30

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VERIFICATION SUMMARY

DATE: 03/26/2002

PATENT APPLICATION: US/10/062,375

TIME: 09:30:32

Input Set : N:\Cr3\RULE60\10062375.raw

Output Set: N:\CRF3\03262002\J062375.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4